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RAW SEQUENCE LISTING

DATE: 08/02/2002

PATENT APPLICATION: US/09/989,981A

TIME: 08:55:39

Input Set : A:\-73-2.app

Output Set: N:\CRF3\08022002\I989981A.raw

3 <110> APPLICANT: Hobbs, Helen H.
4 Shan, Bei
5 Barnes, Robert
6 Tian, Hui
7 Tularik Inc.
8 Board of Regents, The University of Texas System
10 <120> TITLE OF INVENTION: ABCG5 and ABCG8: Compositions and Methods of Use
12 <130> FILE REFERENCE: 018781-007320US
14 <140> CURRENT APPLICATION NUMBER: US 09/989,981A
C--> 15 <141> CURRENT FILING DATE: 2002-07-23
17 <150> PRIOR APPLICATION NUMBER: US 60/252,235
18 <151> PRIOR FILING DATE: 2000-11-20
20 <150> PRIOR APPLICATION NUMBER: US 60/253,645
21 <151> PRIOR FILING DATE: 2000-11-28
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn Ver. 2.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1959
29 <212> TYPE: DNA
30 <213> ORGANISM: Mus musculus
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1959)
35 <223> OTHER INFORMATION: mouse ABCG5 (mABCG5)
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39 Met Gly Glu Leu Pro Phe Leu Ser Pro Glu Gly Ala Arg Gly Pro His
40 1 5 10 15
42 atc aac aga ggg tct ctg agc tcc ctg gag caa ggt tcg gtc acg ggc 96
43 Ile Asn Arg Gly Ser Leu Ser Ser Leu Glu Gln Gly Ser Val Thr Gly
44 20 25 30
46 aca gag gct cgg cac agc tta ggt gtc ctg cat gtg tcc tac agc gtc 144
47 Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val
48 35 40 45
50 agc aac cgt gtc ggg cct tgg tgg aac atc aaa tca tgc cag cag aag 192
51 Ser Asn Arg Val Gly Pro Trp Trp Asn Ile Lys Ser Cys Gln Gln Lys
52 50 55 60
54 tgg gac agg caa atc ctc aaa gat gtc tcc ttg tac atc gag agt ggc 240
55 Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly
56 65 70 75 80
58 cag att atg tgc atc tta ggc agc tca ggc tca ggg aag acc acg ctg 288
59 Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
60 85 90 95

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62 ctg gac gcc atc tcc ggg agg ctg cgg cgc act ggg acc ctg gaa ggg 336
63 Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly
64 100 105 110
66 gag gtg ttt gtg aat ggc tgc gag ctg cgc agg gac cag ttc caa gac 384
67 Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp
68 115 120 125
70 tgc ttc tcc tac gtc ctg cag agc gac gtt ttt ctg agc agc ctc act 432
71 Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr
72 130 135 140
74 gtg cgc gag acg ttg cga tac aca gcg atg ctg gcc ctc tgc cgc agc 480
75 Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser
76 145 150 155 160
78 tcc gcg gac ttc tac aac aag aag gta gag gca gtc atg aca gag ctg 528
79 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
80 165 170 175
82 agc ctg agc cac gtg gcg gac caa atg att ggc agc tat aat ttt ggg 576
83 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly
84 180 185 190
86 gga att tcc agt ggc gag cgg cgc cga gtt tcc atc gca gcc caa ctc 624
87 Gly Ile Ser Ser Gly Glu Arg Arg Arg Val Ser Ile Ala Ala Gln Leu
88 195 200 205
90 ctt cag gac ccc aag gtc atg atg cta gat gag cca acc aca gga ctg 672
91 Leu Gln Asp Pro Lys Val Met Met Leu Asp Glu Pro Thr Thr Gly Leu
92 210 215 220
94 gac tgc atg act gca aat caa att gtc ctt ctc ttg gct gag ctg gct 720
95 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala
96 225 230 235 240
98 cgc agg gac cga att gtg att gtc acc atc cac cag cct cgc tct gag 768
99 Arg Arg Asp Arg Ile Val Ile Val Thr Ile His Gln Pro Arg Ser Glu
100 245 250 255
102 ctc ttc caa cac ttc gac aaa att gcc atc ctg act tac gga gag ttg 816
103 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu
104 260 265 270
106 gtg ttc tgt ggc acc cca gag gag atg ctt ggc ttc ttc aat aac tgt 864
107 Val Phe Cys Gly Thr Pro Glu Glu Met Leu Gly Phe Phe Asn Asn Cys
108 275 280 285
110 ggt tac ccc tgt cct gaa cat tcc aat ccc ttt gat ttt tac atg gac 912
111 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp
112 290 295 300
114 ttg aca tca gtg gac acc caa agc aga gag cgg gaa ata gaa acg tac 960
115 Leu Thr Ser Val Asp Thr Gln Ser Arg Glu Arg Glu Ile Glu Thr Tyr
116 305 310 315 320
118 aag cga gta cag atg ctg gaa tgt gcc ttc aag gaa tct gac atc tat 1008
119 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr
120 325 330 335
122 cac aaa att ctg gag aac att gaa aga gca cga tac ctg aaa acc tta 1056
123 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu
124 340 345 350
126 ccc atg gtt cct ttc aaa aca aaa gat cct cct ggg atg ttc ggc aag 1104

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128			355					360					365				
130	ctt	ggt	gtc	ctg	ctg	agg	cga	gta	aca	aga	aac	tta	atg	agg	aat	aag	1152
131	Leu	Gly	Val	Leu	Leu	Arg	Arg	Val	Thr	Arg	Asn	Leu	Met	Arg	Asn	Lys	
132			370				375					380					
134	cag	gca	gtg	att	atg	cgt	ctc	ggt	cag	aat	ctg	atc	atg	ggc	ctc	ttc	1200
135	Gln	Ala	Val	Ile	Met	Arg	Leu	Val	Gln	Asn	Leu	Ile	Met	Gly	Leu	Phe	
136	385					390					395					400	
138	ctc	att	ttc	tac	ctt	ctc	cgc	gtc	cag	aac	aac	acg	cta	aag	ggc	gct	1248
139	Leu	Ile	Phe	Tyr	Leu	Leu	Arg	Val	Gln	Asn	Asn	Thr	Leu	Lys	Gly	Ala	
140					405					410					415		
142	gtg	cag	gac	cgc	gtg	ggg	ctg	ctc	tat	cag	ctt	gtg	ggt	gcc	acc	cca	1296
143	Val	Gln	Asp	Arg	Val	Gly	Leu	Leu	Tyr	Gln	Leu	Val	Gly	Ala	Thr	Pro	
144				420					425					430			
146	tac	acc	ggc	atg	ctc	aat	gct	gtg	aat	ctg	ttt	ccc	atg	ctg	aga	gcc	1344
147	Tyr	Thr	Gly	Met	Leu	Asn	Ala	Val	Asn	Leu	Phe	Pro	Met	Leu	Arg	Ala	
148			435				440						445				
150	gtc	agc	gac	cag	gag	agt	cag	gat	ggc	ctg	tat	cat	aag	tgg	cag	atg	1392
151	Val	Ser	Asp	Gln	Glu	Ser	Gln	Asp	Gly	Leu	Tyr	His	Lys	Trp	Gln	Met	
152		450				455						460					
154	ctg	ctc	gcc	tac	gtg	cta	cac	gtc	ctc	ccc	ttc	agc	gtc	atc	gcc	acg	1440
155	Leu	Leu	Ala	Tyr	Val	Leu	His	Val	Leu	Pro	Phe	Ser	Val	Ile	Ala	Thr	
156	465				470					475						480	
158	gtc	att	ttc	agc	agt	gtg	tgt	tat	tgg	act	ctg	ggc	ttg	tat	cct	gaa	1488
159	Val	Ile	Phe	Ser	Ser	Val	Cys	Tyr	Trp	Thr	Leu	Gly	Leu	Tyr	Pro	Glu	
160				485					490						495		
162	gtt	gcc	aga	ttt	gga	tat	ttc	tct	gct	gct	ctt	ttg	gcc	cct	cac	tta	1536
163	Val	Ala	Arg	Phe	Gly	Tyr	Phe	Ser	Ala	Ala	Leu	Leu	Ala	Pro	His	Leu	
164			500						505					510			
166	att	gga	gaa	ttt	cta	aca	ctt	gtg	ctg	ctt	ggt	ata	gtc	caa	aac	cct	1584
167	Ile	Gly	Glu	Phe	Leu	Thr	Leu	Val	Leu	Leu	Gly	Ile	Val	Gln	Asn	Pro	
168			515					520					525				
170	aat	att	gtc	aac	agt	ata	gtg	gct	ctg	ctc	agc	atc	tct	ggg	ctg	ctt	1632
171	Asn	Ile	Val	Asn	Ser	Ile	Val	Ala	Leu	Leu	Ser	Ile	Ser	Gly	Leu	Leu	
172		530				535						540					
174	att	gga	tct	gga	ttt	atc	aga	aac	ata	caa	gaa	atg	ccc	att	cct	tta	1680
175	Ile	Gly	Ser	Gly	Phe	Ile	Arg	Asn	Ile	Gln	Glu	Met	Pro	Ile	Pro	Leu	
176	545				550						555					560	
178	aaa	atc	ctg	ggt	tat	ttt	aca	ttc	caa	aaa	tac	tgt	tgt	gag	att	ctc	1728
179	Lys	Ile	Leu	Gly	Tyr	Phe	Thr	Phe	Gln	Lys	Tyr	Cys	Cys	Glu	Ile	Leu	
180				565						570					575		
182	gtg	gtc	aat	gag	ttt	tac	ggc	ctg	aac	ttc	act	tgt	ggt	gga	tcc	aac	1776
183	Val	Val	Asn	Glu	Phe	Tyr	Gly	Leu	Asn	Phe	Thr	Cys	Gly	Gly	Ser	Asn	
184			580						585					590			
186	acc	tct	atg	cta	aat	cac	ccg	atg	tgc	gcc	atc	acc	caa	ggg	gtc	cag	1824
187	Thr	Ser	Met	Leu	Asn	His	Pro	Met	Cys	Ala	Ile	Thr	Gln	Gly	Val	Gln	
188			595					600					605				
190	ttc	atc	gag	aaa	acc	tgc	cca	ggt	gct	aca	tcc	aga	ttc	acg	gca	aac	1872
191	Phe	Ile	Glu	Lys	Thr	Cys	Pro	Gly	Ala	Thr	Ser	Arg	Phe	Thr	Ala	Asn	

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192      610      615      620
194 ttc ctc atc tta tat ggg ttt atc cca gct ctg gtc atc cta gga ata 1920
195 Phe Leu Ile Leu Tyr Gly Phe Ile Pro Ala Leu Val Ile Leu Gly Ile
196 625      630      635      640
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216 Thr Glu Ala Arg His Ser Leu Gly Val Leu His Val Ser Tyr Ser Val
217 35 40 45
218 Ser Asn Arg Val Gly Pro Trp Asn Ile Lys Ser Cys Gln Gln Lys
219 50 55 60
220 Trp Asp Arg Gln Ile Leu Lys Asp Val Ser Leu Tyr Ile Glu Ser Gly
221 65 70 75 80
222 Gln Ile Met Cys Ile Leu Gly Ser Ser Gly Ser Gly Lys Thr Thr Leu
223 85 90 95
224 Leu Asp Ala Ile Ser Gly Arg Leu Arg Arg Thr Gly Thr Leu Glu Gly
225 100 105 110
226 Glu Val Phe Val Asn Gly Cys Glu Leu Arg Arg Asp Gln Phe Gln Asp
227 115 120 125
228 Cys Phe Ser Tyr Val Leu Gln Ser Asp Val Phe Leu Ser Ser Leu Thr
229 130 135 140
230 Val Arg Glu Thr Leu Arg Tyr Thr Ala Met Leu Ala Leu Cys Arg Ser
231 145 150 155 160
232 Ser Ala Asp Phe Tyr Asn Lys Lys Val Glu Ala Val Met Thr Glu Leu
233 165 170 175
234 Ser Leu Ser His Val Ala Asp Gln Met Ile Gly Ser Tyr Asn Phe Gly
235 180 185 190
236 Gly Ile Ser Ser Gly Glu Arg Arg Val Ser Ile Ala Ala Gln Leu
237 195 200 205
238 Leu Gln Asp Pro Lys Val Met Met Leu Asp Glu Pro Thr Thr Gly Leu
239 210 215 220
240 Asp Cys Met Thr Ala Asn Gln Ile Val Leu Leu Leu Ala Glu Leu Ala
241 225 230 235 240
242 Arg Arg Asp Arg Ile Val Ile Val Thr Ile His Gln Pro Arg Ser Glu
243 245 250 255
244 Leu Phe Gln His Phe Asp Lys Ile Ala Ile Leu Thr Tyr Gly Glu Leu
245 260 265 270
246 Val Phe Cys Gly Thr Pro Glu Glu Met Leu Gly Phe Phe Asn Asn Cys

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247          275          280          285
248 Gly Tyr Pro Cys Pro Glu His Ser Asn Pro Phe Asp Phe Tyr Met Asp
249          290          295          300
250 Leu Thr Ser Val Asp Thr Gln Ser Arg Glu Arg Glu Ile Glu Thr Tyr
251 305          310          315          320
252 Lys Arg Val Gln Met Leu Glu Cys Ala Phe Lys Glu Ser Asp Ile Tyr
253          325          330          335
254 His Lys Ile Leu Glu Asn Ile Glu Arg Ala Arg Tyr Leu Lys Thr Leu
255          340          345          350
256 Pro Met Val Pro Phe Lys Thr Lys Asp Pro Pro Gly Met Phe Gly Lys
257          355          360          365
258 Leu Gly Val Leu Leu Arg Arg Val Thr Arg Asn Leu Met Arg Asn Lys
259          370          375          380
260 Gln Ala Val Ile Met Arg Leu Val Gln Asn Leu Ile Met Gly Leu Phe
261 385          390          395          400
262 Leu Ile Phe Tyr Leu Leu Arg Val Gln Asn Asn Thr Leu Lys Gly Ala
263          405          410          415
264 Val Gln Asp Arg Val Gly Leu Leu Tyr Gln Leu Val Gly Ala Thr Pro
265          420          425          430
266 Tyr Thr Gly Met Leu Asn Ala Val Asn Leu Phe Pro Met Leu Arg Ala
267          435          440          445
268 Val Ser Asp Gln Glu Ser Gln Asp Gly Leu Tyr His Lys Trp Gln Met
269          450          455          460
270 Leu Leu Ala Tyr Val Leu His Val Leu Pro Phe Ser Val Ile Ala Thr
271 465          470          475          480
272 Val Ile Phe Ser Ser Val Cys Tyr Trp Thr Leu Gly Leu Tyr Pro Glu
273          485          490          495
274 Val Ala Arg Phe Gly Tyr Phe Ser Ala Ala Leu Leu Ala Pro His Leu
275          500          505          510
276 Ile Gly Glu Phe Leu Thr Leu Val Leu Leu Gly Ile Val Gln Asn Pro
277          515          520          525
278 Asn Ile Val Asn Ser Ile Val Ala Leu Leu Ser Ile Ser Gly Leu Leu
279          530          535          540
280 Ile Gly Ser Gly Phe Ile Arg Asn Ile Gln Glu Met Pro Ile Pro Leu
281 545          550          555          560
282 Lys Ile Leu Gly Tyr Phe Thr Phe Gln Lys Tyr Cys Cys Glu Ile Leu
283          565          570          575
284 Val Val Asn Glu Phe Tyr Gly Leu Asn Phe Thr Cys Gly Gly Ser Asn
285          580          585          590
286 Thr Ser Met Leu Asn His Pro Met Cys Ala Ile Thr Gln Gly Val Gln
287          595          600          605
288 Phe Ile Glu Lys Thr Cys Pro Gly Ala Thr Ser Arg Phe Thr Ala Asn
289          610          615          620
290 Phe Leu Ile Leu Tyr Gly Phe Ile Pro Ala Leu Val Ile Leu Gly Ile
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293          645          650
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VERIFICATION SUMMARY

DATE: 08/02/2002

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Input Set : A:\-73-2.app

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date